

OIEP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/909,672

DATE: 07/30/2001

TIME: 15:46:24

Input Set : A:\LeA34771.app

Output Set: N:\CRF3\07302001\I909672.raw

3 <110> APPLICANT: Bayer Aktiengesellschaft

5 <120> TITLE OF INVENTION: Ultraspinal protein from *Heliothis virescens*

7 <130> FILE REFERENCE: Le A 34 774

C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/909,672

C--> 10 <141> CURRENT FILING DATE: 2001-07-20

12 <150> PRIOR APPLICATION NUMBER: DE 100 36 469.1

13 <151> PRIOR FILING DATE: 2000-07-25

15 <160> NUMBER OF SEQ ID NOS: 2

17 <170> SOFTWARE: PatentIn Ver. 2.1

19 <210> SEQ ID NO: 1

20 <211> LENGTH: 1398

21 <212> TYPE: DNA

22 <213> ORGANISM: *Heliothis virescens*

24 <220> FEATURE:

25 <221> NAME/KEY: CDS

26 <222> LOCATION: (1)..(1398)

28 <400> SEQUENCE: 1

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30	Met Ser Val Ala Lys Lys Asp Lys Pro Thr Met Ser Val Thr Ala Leu	
31	1 5 10 15	
33	atc aac tgg gct cga ccc ttg ccg ccg ggc caa cag cag cag ccg atg	96
34	Ile Asn Trp Ala Arg Pro Leu Pro Pro Gly Gln Gln Gln Gln Pro Met	
35	20 25 30	
37	acg cct acg tcg ccc gga aac atg ctt caa ccg atg gct acg ccg tct	144
38	Thr Pro Thr Ser Pro Gly Asn Met Leu Gln Pro Met Ala Thr Pro Ser	
39	35 40 45	
41	aac tta ccg act gtc gac tgc tca ctc gat att caa tgg cta aac ttg	192
42	Asn Leu Pro Thr Val Asp Cys Ser Leu Asp Ile Gln Trp Leu Asn Leu	
43	50 55 60	
45	gag gga ggt ttt atg tcg ccg atg tca ccg ccg gag atg aag cca gac	240
46	Glu Gly Gly Phe Met Ser Pro Met Ser Pro Pro Glu Met Lys Pro Asp	
47	65 70 75 80	
49	acg gcg atg cta gac ggc ctg cga gac gac tcc acc cca ccc cca gct	288
50	Thr Ala Met Leu Asp Gly Leu Arg Asp Ser Thr Pro Pro Pro Ala	
51	85 90 95	
53	ttc aag aac tac ccc ccg aac cat ccc cta agt ggt tct aag cac ctc	336
54	Phe Lys Asn Tyr Pro Pro Asn His Pro Leu Ser Gly Ser Lys His Leu	
55	100 105 110	
57	tgt tct ata tgt gga gat aga gcg tcg ggg aaa cat tat gga gta tac	384
58	Cys Ser Ile Cys Gly Asp Arg Ala Ser Gly Lys His Tyr Gly Val Tyr	
59	115 120 125	
61	agt tgt gaa ggt tgc aaa ggt ttc ttc aaa agg acg gta aga aaa gac	432
62	Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asp	
63	130 135 140	
65	tta acg tac gca tgc cgc gaa gaa cgt aac tgc atc ata gac aaa cgc	480
66	Leu Thr Tyr Ala Cys Arg Glu Glu Arg Asn Cys Ile Ile Asp Lys Arg	
67	145 150 155 160	

ENTERED

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69 cag agg aac aga tgc cag tac tgt agg tac cag aaa tgt ctc gcg tgc 528
70 Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys Cys Leu Ala Cys
71 165 170 175 ~
73 ggc atg aag agg gaa gcg gtg cag gag gag agg cag agg gcc gcc aga 576
74 Gly Met Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Ala Ala Arg
75 180 185 190
77 ggt acg gag gat gca cat ccg agc agc tcg gtg cag gta cag gag tta 624
78 Gly Thr Glu Asp Ala His Pro Ser Ser Ser Val Gln Val Gln Glu Leu
79 195 200 205
81 tca atc gag cgg ttg ctg gag atg gag tca ctg gta gct gac ccc agc 672
82 Ser Ile Glu Arg Leu Leu Glu Met Glu Ser Leu Val Ala Asp Pro Ser
83 210 215 220
85 gaa gag ttc cag ttc ctt cgt gtg gga ccc gac agt aat gtg ccg cct 720
86 Glu Glu Phe Gln Phe Leu Arg Val Gly Pro Asp Ser Asn Val Pro Pro
87 225 230 235 240
89 aag ttc cgc gcc cct gtc tcc agc ctt tgt caa ata ggc aac aaa caa 768
90 Lys Phe Arg Ala Pro Val Ser Ser Leu Cys Gln Ile Gly Asn Lys Gln
91 245 250 255
93 ata gcg gcg cta gtg gtg tgg gcg cgc gac atc ccg cac ttc agc cag 816
94 Ile Ala Ala Leu Val Val Trp Ala Arg Asp Ile Pro His Phe Ser Gln
95 260 265 270
97 ctt gag atg gaa gac cag atc ctg ctc atc aaa ggc tcc tgg aac gaa 864
98 Leu Glu Met Glu Asp Gln Ile Leu Leu Ile Lys Gly Ser Trp Asn Glu
99 275 280 285
101 ctg ctg ctc ttc gcc att gcg tgg cgg tct atg gag ttc ctg aca gaa 912
102 Leu Leu Leu Phe Ala Ile Ala Trp Arg Ser Met Glu Phe Leu Thr Glu
103 290 295 300
105 gag cga gac ggc gtg gac ggc act ggg aac aga acc aca tcg ccg cca 960
106 Glu Arg Asp Gly Val Asp Gly Thr Gly Asn Arg Thr Thr Ser Pro Pro
107 305 310 315 320
109 caa ctt atg tgt ctc atg cct ggc atg acg ctg cac cgc aac tca gcg 1008
110 Gln Leu Met Cys Leu Met Pro Gly Met Thr Leu His Arg Asn Ser Ala
111 325 330 335
113 ctg cag gcg ggc gtg ggg cag atc ttc gac cgc gtg ctg tcg gag ctg 1056
114 Leu Gln Ala Gly Val Gly Gln Ile Phe Asp Arg Val Leu Ser Glu Leu
115 340 345 350
117 tcg ctg aag atg cgc acc ctg cgc gtc gac cag gcc gag tac gtc gcg 1104
118 Ser Leu Lys Met Arg Thr Leu Arg Val Asp Gln Ala Glu Tyr Val Ala
119 355 360 365
121 ctc aag gcc atc ata ctg ctc aac cca gat gtg aag gga ctg aaa aac 1152
122 Leu Lys Ala Ile Ile Leu Leu Asn Pro Asp Val Lys Gly Leu Lys Asn
123 370 375 380
125 agg caa gaa gtg gaa gtt tta cga gaa aag atg ttc ctg tgc ctg gac 1200
126 Arg Gln Glu Val Glu Val Leu Arg Glu Lys Met Phe Leu Cys Leu Asp
127 385 390 395 400
129 gag tac tgc cgc cgc tcg cgc agt tcg gag gag ggt cgg ttc gcg gcg 1248
130 Glu Tyr Cys Arg Arg Ser Arg Ser Ser Glu Glu Gly Arg Phe Ala Ala
131 405 410 415
133 ctg ctg ctg cgc ctg ccc gcg tta cgt tcc att tca ctc aag agc ttc 1296

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134 Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Ser Leu Lys Ser Phe
135          420          425          430
137 gag cac ctg ttc ttc cac ctg gtg gcc gac acc agc atc gcc ggc 1344
138 Glu His Leu Phe Phe Phe His Leu Val Ala Asp Thr Ser Ile Ala Gly
139          435          440          445
141 tac atc cgc gac gcg ctg cgc aac cac gcg ccg ccc atc gac acc aac 1392
142 Tyr Ile Arg Asp Ala Leu Arg Asn His Ala Pro Pro Ile Asp Thr Asn
143          450          455          460
145 atg atg 1398
146 Met Met
147 465
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151 <211> LENGTH: 466
152 <212> TYPE: PRT
153 <213> ORGANISM: Heliothis virescens
155 <400> SEQUENCE: 2
156 Met Ser Val Ala Lys Lys Asp Lys Pro Thr Met Ser Val Thr Ala Leu
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159 Ile Asn Trp Ala Arg Pro Leu Pro Pro Gly Gln Gln Gln Gln Pro Met
160 20 25 30
162 Thr Pro Thr Ser Pro Gly Asn Met Leu Gln Pro Met Ala Thr Pro Ser
163 35 40 45
165 Asn Leu Pro Thr Val Asp Cys Ser Leu Asp Ile Gln Trp Leu Asn Leu
166 50 55 60
168 Glu Gly Gly Phe Met Ser Pro Met Ser Pro Pro Glu Met Lys Pro Asp
169 65 70 75 80
171 Thr Ala Met Leu Asp Gly Leu Arg Asp Asp Ser Thr Pro Pro Pro Ala
172 85 90 95
174 Phe Lys Asn Tyr Pro Pro Asn His Pro Leu Ser Gly Ser Lys His Leu
175 100 105 110
177 Cys Ser Ile Cys Gly Asp Arg Ala Ser Gly Lys His Tyr Gly Val Tyr
178 115 120 125
180 Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asp
181 130 135 140
183 Leu Thr Tyr Ala Cys Arg Glu Glu Arg Asn Cys Ile Ile Asp Lys Arg
184 145 150 155 160
186 Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys Cys Leu Ala Cys
187 165 170 175
189 Gly Met Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Ala Ala Arg
190 180 185 190
192 Gly Thr Glu Asp Ala His Pro Ser Ser Ser Val Gln Val Gln Glu Leu
193 195 200 205
195 Ser Ile Glu Arg Leu Leu Glu Met Glu Ser Leu Val Ala Asp Pro Ser
196 210 215 220
198 Glu Glu Phe Gln Phe Leu Arg Val Gly Pro Asp Ser Asn Val Pro Pro
199 225 230 235 240
201 Lys Phe Arg Ala Pro Val Ser Ser Leu Cys Gln Ile Gly Asn Lys Gln
202 245 250 255
204 Ile Ala Ala Leu Val Val Trp Ala Arg Asp Ile Pro His Phe Ser Gln

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205          260          265          270
207 Leu Glu Met Glu Asp Gln Ile Leu Leu Ile Lys Gly Ser Trp Asn Glu
208          275          280          285
210 Leu Leu Leu Phe Ala Ile Ala Trp Arg Ser Met Glu Phe Leu Thr Glu
211          290          295          300
213 Glu Arg Asp Gly Val Asp Gly Thr Gly Asn Arg Thr Thr Ser Pro Pro
214 305          310          315          320
216 Gln Leu Met Cys Leu Met Pro Gly Met Thr Leu His Arg Asn Ser Ala
217          325          330          335
219 Leu Gln Ala Gly Val Gly Gln Ile Phe Asp Arg Val Leu Ser Glu Leu
220          340          345          350
222 Ser Leu Lys Met Arg Thr Leu Arg Val Asp Gln Ala Glu Tyr Val Ala
223          355          360          365
225 Leu Lys Ala Ile Ile Leu Leu Asn Pro Asp Val Lys Gly Leu Lys Asn
226          370          375          380
228 Arg Gln Glu Val Glu Val Leu Arg Glu Lys Met Phe Leu Cys Leu Asp
229 385          390          395          400
231 Glu Tyr Cys Arg Arg Ser Arg Ser Ser Glu Glu Gly Arg Phe Ala Ala
232          405          410          415
234 Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Ser Leu Lys Ser Phe
235          420          425          430
237 Glu His Leu Phe Phe Phe His Leu Val Ala Asp Thr Ser Ile Ala Gly
238          435          440          445
240 Tyr Ile Arg Asp Ala Leu Arg Asn His Ala Pro Pro Ile Asp Thr Asn
241          450          455          460
243 Met Met
244 465

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VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date